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=> s rad51 (p) gene

             5 RAD51
         21722 GENE
         16104 GENES
         23370 GENE
                 (GENE OR GENES)
L1           3 RAD51 (P) GENE

=> d 1-3 bib ab kwic
```

L1: 1 of 3

US PAT NO: 5,811,231 [IMAGE AVAILABLE]
DATE ISSUED: Sep. 22, 1998
TITLE: Methods and kits for eukaryotic gene profiling
INVENTOR: Spencer B. Farr, Longmont, CO
Marque D. Todd, Westminster, CO
ASSIGNEE: Pres. and Fellows of Harvard College, Cambridge, MA (U.S. corp.)
Xenometrix, Inc. (U.S. corp.)
APPL-NO: 08/374,641
DATE FILED: Jul. 21, 1995
ART-UNIT: 187
PRIM-EXMR: W. Gary Jones
ASST-EXMR: Dianne Rees
LEGAL-REP: James F. Haley, Jr., Esq., Andrew S. Marks, Esq.

L1: 1 of 3

US PAT NO: 5,811,231 [IMAGE AVAILABLE]

ABSTRACT:

This invention provides methods and diagnostic kits for identifying and characterizing toxic compounds. These methods and diagnostic kits measure transcription or translation levels from genes linked to native eukaryotic stress promoters, especially those of mammals. The kits and methods of this invention utilize at least one stress promoter from each of the following groups: redox stress, DNA stress, protein stress and energy/ionic stress. The invention also provides methods and diagnostic kits for identifying and characterizing compounds that are toxic to specific organs, such as skin and the eye, as well as for each of the individual stresses indicated above. The methods and diagnostic kits of this invention yield information concerning the action of a compound on a subcellular level. This information may be utilized to design antitoxins to compounds found to be toxic and in active drug design.

DETDESC:

DETD(69)

Also, a large number of DNA stress **genes** have been identified and sequenced in yeast. These include MAG, the methyladenine DNA glycosylase, and MGT1, which respond to DNA alkylation damage [W. Xiao et al., Mol. Cell. Biol., 13, pp. 7213-21 (1993)]; **RAD51**, RAD54, RAD6, RAD23, RAD2, RAD18 and RAD7, all of which respond to DNA strand breaks [G.

Basile et al., Mol.. . . by DNA damage [S. J. Elledge et al., Mol. Cell. Biol., 9, pp. 5373-86 (1989); S. J. Elledge et al., **Gene** Dev., 4, pp. 740-51 (1990); Z. Zhou et al., Genetics, 131, pp. 851-66 (1992)]; CDC9, the yeast DNA ligase [T. A. Peterson et al., Mol. Cell. Biol., 5, pp. 226-35 (1985)]; UBI4, another **gene** that responds to DNA damage [J. M. Treger et al., Mol. Cell. Biol., 8, pp. 1132-36 (1988)]; and DDR48, a **gene** which responds to mutagens [J. M. Treger et al., Mol. Cell. Biol., 10, pp. 3174-84 (1990)]. In addition, several other DNA stress **genes** have also been identified in yeast [G. W. Robinson et al., Proc. Natl. Acad. Sci. USA, 83, pp. 1842-46 (1986);. . .

L1: 2 of 3

US PAT NO: 5,780,296 [IMAGE AVAILABLE]
DATE ISSUED: Jul. 14, 1998
TITLE: Compositions and methods to promote homologous recombination in eukaryotic cells and organisms

INVENTOR: William K. Holloman, Yorktown Heights, NY
Eric B. Kmiec, Malvern, PA

ASSIGNEE: Thomas Jefferson University, Philadelphia, PA (U.S. corp.)
APPL-NO: 08/373,134
DATE FILED: Jan. 17, 1995
ART-UNIT: 184
PRIM-EXMR: Eric Grimes
LEGAL-REP: Daniel Hansburg

L1: 2 of 3

US PAT NO: 5,780,296 [IMAGE AVAILABLE]

ABSTRACT:
The invention concerns genes encoding recombinases that can be used to promote homologous recombination in eukaryotic cells and expression vectors that can be used to transiently express recombinases in target cells. One embodiment of the invention encompasses genetically engineered nucleic acids that encode a non-naturally occurring recombinase that causes a greater rate of recombination than does the naturally occurring recombinase. Recombinases from Ustilago maydis, Saccharomyces cerevisiae are specifically included in the invention.

DETDESC:

DETD(12)

Alternative methods to isolate putative REC2 **genes** from other species of eukaryotes utilize the paired sense and antisense oligonucleotides, the sequences of which encode, or are complementary. . conserved among species. One such portion consists of residues 226-270, which shows homology with S. cerevisiae proteins Dmc1, Rad57 and **Rad51** and with the E. coli protein RecA. The oligonucleotides are selected to bracket portions of the **gene** of about 100 to 500 bp. The paired oligonucleotides can be used as primers in a polymerase chain reaction (PCR) to amplify the bracketed fragment of the **gene**. The amplification products may then be cloned, sequenced and those, the sequence of which indicates that they are fragments of a Rec2 **gene**, can be used as probes to isolate the entire **gene** from a suitable library.

L1: 3 of 3

US PAT NO: 5,707,811 [IMAGE AVAILABLE]
DATE ISSUED: Jan. 13, 1998
TITLE: Reca-assisted cloning of DNA
INVENTOR: Lance Joseph Ferrin, Gaithersburg, MD

	R. Daniel Camerini-Otero, Kensington, MD
ASSIGNEE:	The United States of America as represented by the Secretary of Health and Human Services, Washington, DC (U.S. corp.)
APPL-NO:	08/682,305
DATE FILED:	Jul. 17, 1996
ART-UNIT:	187
PRIM-EXMR:	W. Gary Jones
ASST-EXMR:	Amy Atzel
LEGAL-REP:	Knobbe, Martens, Olson & Bear, LLP

US PAT NO: 5,707,811 [IMAGE AVAILABLE] L1: 3 of 3

ABSTRACT:
DNA is cloned and labeled in a sequence-specific manner. The DNA is digested with one or more restriction enzymes which produce 3' recessed ends. A desired fragment is protected from elongation by DNA polymerase by addition of E. coli RecA protein and oligonucleotides about 30 to 60 bases in length complementary to the 3' recessed ends of the digested fragment. RecA and DNA polymerase are then inactivated, leaving only the desired fragment with 3' recessed ends which is then ligated into a vector containing complementary 3' recessed ends.

DETDESC:

DETD(47)

Multiple . . . clones were selected on chloramphenicol plates to eliminate any background from the previous plasmid vector which contained an ampicillin resistance **gene**. This demonstrated an additional 500-fold enrichment and showed that incorrect clones arose mainly through a stochastic process, and not through. . . partial homology to the int-2 sequence. A 1.2 kb EcoRI-BamHI yeast genomic DNA fragment containing the proximal portion of the **RAD51 gene** (Shmohara et al., Cell 69:457, 1992) was also cloned. The oligonucleotides used to clone this fragment had sequences complementary to. . .

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L1          366 RAD51 AND GENE

=> s l1 and sequence
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L2 186 L1 AND SEQUENCE

=> s rad51 (2a) gene (2a) sequence

1 FILES SEARCHED...
L3 4 RAD51 (2A) GENE (2A) SEQUENCE

=> d 1-4 bib ab

L3 ANSWER 1 OF 4 MEDLINE
AN 1998110585 MEDLINE
DN 98110585
TI Identification of a novel human RAD51 homolog, RAD51B [published erratum appears in Genomics 1998 Aug 1;51(3):480].
AU Albala J S; Thelen M P; Prange C; Fan W; Christensen M; Thompson L H; Lennon G G
CS Biology and Biotechnology Research Program, Lawrence Livermore National Laboratory, California 95441-0808, USA.. albala1@llnl.gov
SO GENOMICS, (1997 Dec 15) 46 (3) 476-9.
Journal code: GEN. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U84138
EM 199805
AB The highly conserved Saccharomyces cerevisiae RAD51 protein functions in both mitotic and meiotic homologous recombination and in double-strand break repair. Screening of the public cDNA **sequence** database for **RAD51**-like **genes** led to the identification of a partial sequence from a breast tissue library present in the I.M.A.G.E. (Integrated Molecular Analysis of Genes and their Expression) collection. An extended 1764-bp cDNA clone encoding an open reading frame of 350 amino acids was isolated. This clone showed significant amino acid identity with other human RAD51 homologs. The new homolog, named RAD51B, was mapped to human chromosome 14q23-q24.2 using a panel of human-hamster somatic cell hybrids and fluorescence in situ hybridization. Northern blot analysis demonstrated that RAD51B mRNA is widely expressed and most abundant in tissues active in recombination. Functions associated with known RAD51 homologs suggest a role for RAD51B in meiotic recombination and/or recombinational repair.

L3 ANSWER 2 OF 4 MEDLINE
AN 92318940 MEDLINE
DN 92318940
TI Semidominant suppressors of Srs2 helicase mutations of Saccharomyces cerevisiae map in the **RAD51 gene**, whose **sequence** predicts a protein with similarities to procaryotic RecA proteins.
AU Aboussekhra A; Chanet R; Adjiri A; Fabre F
CS Section de Biologie, Instiut Curie, Centre Universitaire, Orsay, France..
SO MOLECULAR AND CELLULAR BIOLOGY, (1992 Jul) 12 (7) 3224-34.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)

LA English
FS Priority Journals
OS GENBANK-X64270
EM 199210
AB Eleven suppressors of the radiation sensitivity of Saccharomyces cerevisiae diploids lacking the Srs2 helicase were analyzed and found to contain codominant mutations in the RAD51 gene known to be involved in recombinational repair and in genetic recombination. These mutant alleles confer an almost complete block in recombinational repair, as does deletion of RAD51, but heterozygous mutant alleles suppress the defects of srs2::LEU2 cells and are semidominant in Srs2+ cells. The results of this study are interpreted to mean that wild-type Rad51 protein binds to single-stranded DNA and that the semidominant mutations do not prevent this binding. The cloning and sequencing of RAD51 indicated that the gene encodes a predicted 400-amino-acid protein with a molecular mass of 43 kDa. Sequence comparisons revealed homologies to domains of Escherichia coli RecA protein predicted to be involved in DNA binding, ATP binding, and ATP hydrolysis. The expression of RAD51, measured with a RAD51-lacZ gene fusion, was found to be UV- and gamma-ray-inducible, with dose-dependent responses.

L3 ANSWER 3 OF 4 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1998:93459 BIOSIS
DN PREV199800093459
TI Identification of a novel human RAD51 homolog, RAD51B.
AU Albala, Joanna S. (1); Thelen, Michael P.; Prange, Christa; Fan, Wufang; Christensen, Mari; Thompson, Larry H.; Lennon, Gregory G.
CS (1) Biology Biotechnol. Res. Program, Lawrence Livermore Natl. Lab., 7000 East Avenue L-452, Livermore, CA 94550 USA
SO Genomics, (Dec. 15, 1997) Vol. 46, No. 3, pp. 476-479.
ISSN: 0888-7543.
DT Article
LA English
AB The highly conserved Saccharomyces cerevisiae RAD51 protein functions in both mitotic and meiotic homologous recombination and in double-strand break repair. Screening of the public cDNA **sequence** database for **RAD51**-like **genes** led to the identification of a partial sequence from a breast tissue library present in the I.M.A.G.E. (Integrated Molecular Analysis of Genes and their Expression) collection. An extended 1764-bp cDNA clone encoding an open reading frame of 350 amino acids was isolated. This clone showed significant amino acid identity with other human RAD51 homologs. The new homolog, named RAD51B, was mapped to human chromosome 14q23-q24.2 using a panel of human-hamster somatic cell hybrids and fluorescence in situ hybridization. Northern blot analysis demonstrated that RAD51B mRNA is widely expressed and most abundant in tissues active in recombination. Functions associated with known RAD51 homologs suggest a role for RAD51B in meiotic recombination and/or recombinational repair.

L3 ANSWER 4 OF 4 BIOSIS COPYRIGHT 1999 BIOSIS
AN 1992:410204 BIOSIS
DN BA94:73404
TI SEMIDOMINANT SUPPRESSORS OF SRS2 HELICASE MUTATIONS OF SACCHAROMYCES-CEREVISIAE MAP IN THE **RAD51 GENE** WHOSE **SEQUENCE** PREDICTS A PROTEIN WITH SIMILARITIES TO PROCARYOTIC RECA PROTEINS.
AU ABOUSSEKHRA A; CHANET R; ADJIRI A; FABRE F

CS SECT. BIOL., INST. CURIE, BATIMENT 110, CENT. UNIV., 91405 ORSAY CEDEX, FR.

SO MOL CELL BIOL, (1992) 12 (7), 3224-3234.
CODEN: MCEBD4. ISSN: 0270-7306.

FS BA; OLD

LA English

AB Eleven suppressors of the radiation sensitivity of Saccharomyces cervisiae diploids lacking the Srs2 helicase were analyzed and found to contain codominant mutations in the RAD51 gene known to be involved in recombinational repair and in genetic recombination. These mutant alleles confer and almost complete block in recombinational repair, as does deletion of RAD51, but heterozygous mutant alleles suppress the defects of srs2::LEU2 cells an are semidominant in Srs2+ cells. The results of this study are interpreted to mean that wild-type Rad51 protein binds to single-stranded DNA and that the semidominant mutations do not prevent this binding. The cloning and sequencing of RAD51 indicated that the gene encodes a predicted 400-amino-acid protein with a molecular mass of 43 kDa. Sequence comparisons revealed homologies to domain of Escherichia coli RecA protein pedicted to be involved in DNA binding, ATP binding, and ATP hydrolysis. The expression of RAD51, measured with a RAD51-lacZ gene fusion, was found to be UV- and .gamma.-ray-inducible, with dose-dependent responses.

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